

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102030_us-10-714-389-52.sl.rng.

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This page gives you Search Results detail for the Application 10714389 and Search Result 20070807_102030_us-10-714-389-52.sl.rng.

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10/714,389

OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 10:13:07 ; Search time 444 Seconds
(without alignments)
6325.687 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 actttgccaagcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score over Length	% Query Match Length	DB	ID	Description
1	379	100.0	100.0	379	4 AAH55527	Aah55527 Hu
2	379	100.0	100.0	379	7 ADU01271	Adu01271 Br
3	379	100.0	100.0	379	7 ADZ41535	Adz41535 Hu
4	379	100.0	100.0	379	12 ADN40297	Adn40297 Hu

ALIGNMENTS

RESULT 1

AAH55527

ID AAH55527 standard; DNA; 379 BP.

XX

AC AAH55527;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human breast tumour protein contig 11 DNA sequence.

XX

KW Cytostatic; vaccine; human; breast tumour protein; breast cancer;
KW gene therapy; ds.

XX

OS Homo sapiens.

XX

PN WO200140269-A2.

XX

PD 07-JUN-2001.

XX

PF 29-NOV-2000; 2000WO-US032520.

XX

PR 30-NOV-1999; 99US-00451651.

PR 22-FEB-2000; 2000US-00510662.

PR 10-MAR-2000; 2000US-00523586.

PR 07-APR-2000; 2000US-00545068.

PR 15-MAY-2000; 2000US-00571025.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

XX

DR WPI; 2001-356154/37.

XX

PT Breast tumor polypeptides and the nucleic acids that encode them, useful
PT for the prevention, diagnosis and treatment of breast cancer.

XX

PS Claim 24; Page 139; 221pp; English.

XX

CC The present sequence is a human breast tumour protein coding sequence.

CC This sequence may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the breast tumour

CC protein e.g. breast cancer. For example, this sequence may be used to

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102031_us-10-714-389-52.sl.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 10:47:25 ; Search time 2785 Seconds
(without alignments)
9406.317 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 actttgcccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score over		% Query				ID	Description
	Score	Length	Match	Length	DB			
1	379	100.0	100.0	379	2	CS110385	CS110385 Se	
2	379	100.0	100.0	379	2	AX156195	AX156195 Se	

ALIGNMENTS

RESULT 1

CS110385

LOCUS CS110385 379 bp DNA linear PAT 22-JUN-2005

DEFINITION Sequence 52 from Patent WO2005051990.

ACCESSION CS110385

VERSION CS110385.1 GI:68148583

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Dillon, D.C. and Jiang, Y.

TITLE Compositions and methods for the therapy and diagnosis of breast cancer

JOURNAL Patent: WO 2005051990-A 52 09-JUN-2005;

Corixa Corporation (US)

FEATURES

source Location/Qualifiers

1. .379

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 379; DB 2; Length 379;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 4.4e-109;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTTCATGTCCTGCAA 60
        |||
Db      1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTTCATGTCCTGCAA 60

Qy      61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTCGCG 120
        |||
Db      61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTCGCG 120

Qy      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180
        |||
Db      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180

Qy      181 TTAGCTTATCCTTAAGAGACTCCTTCCGGTCTGGATTACTTTCTCTGTGAAGTATGATGAA 240
        |||
Db      181 TTAGCTTATCCTTAAGAGACTCCTTCCGGTCTGGATTACTTTCTCTGTGAAGTATGATGAA 240

```

**SCORE Search Results Details for Application
10714389 and Search Result
20070807_102033_us-10-714-389-52.sl.rst.**

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SCORE System Overview

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 10:49:12 ; Search time 4854 Seconds
(without alignments)
4844.159 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 0

```
Minimum DB seq length: 20
Maximum DB seq length: 379
```

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

```
Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_gss1:*
16: gb_gss2:*
```

17: gb_gss3:*
18: gb_gss4:*
19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	%					
No.	Score	Length	Match	Length	DB	ID	Description

No matches found

Search completed: August 8, 2007, 12:10:19
Job time : 4854 secs

SCORE 3.0 BuildDate: 10/17/2007

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 11:20:44 ; Search time 235 Seconds
(without alignments)
5827.613 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 actttgcccaagcagtaaagg.....ttcaggtatgagtcagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	%					
No.	Score	Length	Match	Length	DB	ID	Description

No matches found

Search completed: August 8, 2007, 16:33:11
Job time : 235 secs

SCORE 3.0 BuildDate: 10/17/2007

SCORE Search Results Details for Application 10714389 and Search Result 20070807_102038_us-10-714-389-52.sl.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 11:32:35 ; Search time 929 Seconds
(without alignments)
5012.932 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 acttttgccaagcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score over Length	% Query Match	Length	DB	ID	Description
1	379	100.0	100.0	379	3	US-09-778-320-52	Sequence 5
2	379	100.0	100.0	379	3	US-09-910-689-52	Sequence 5
3	379	100.0	100.0	379	6	US-10-010-742-52	Sequence 5
4	379	100.0	100.0	379	8	US-10-714-389-52	Sequence 5
5	379	100.0	100.0	379	8	US-10-717-296-52	Sequence 5

ALIGNMENTS

RESULT 1

US-09-778-320-52

; Sequence 52, Application US/09778320

; Patent No. US20010034052A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Day, Craig H.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Wang, TongTong

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.491C5

; CURRENT APPLICATION NUMBER: US/09/778,320

; CURRENT FILING DATE: 2001-02-06

; NUMBER OF SEQ ID NOS: 301

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 52

; LENGTH: 379

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-778-320-52

Query Match 100.0%; Score 379; DB 3; Length 379;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 8.3e-104;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTGCATGTCCTGCAA 60
        |||
Db      1 ACTTTGCCAAGCAGTAAAGGATCCAGGAGATAGCACTGGATGTGGTGTGCATGTCCTGCAA 60

Qy      61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTCGCG 120
        |||
Db      61 ACATGAACGTTTTCACTTCAGCCTGGAGATCTGCTTCAGAGAAATCTTTGGTGTTCGCG 120

Qy      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180
        |||
Db      121 TTTTGGCACTCAAAAGTATGTCCAGAAAATCCCAGCGCCTTTTCTGAGTAGTATCTTGTT 180

```

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2007, 11:34:20 ; Search time 1211 Seconds
(without alignments)
3373.664 Million cell updates/sec

Title: US-10-714-389-52
Perfect score: 379
Sequence: 1 actttgcccaagcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16529674 seqs, 5389851713 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 20
Maximum DB seq length: 379

Post-processing: Minimum Score over Length 100%
Listing first 100 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
- 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
- 12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
- 13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*

17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
 18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
 19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
 20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq7:*
 21: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq8:*
 22: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Score over Length	% Match	Query Length	DB	ID	Description
c 1	32	100.0	8.4	32	6	US-10-535-164-282627	Sequence 2
c 2	32	100.0	8.4	32	11	US-10-536-560-79632	Sequence 7
c 3	32	100.0	8.4	32	11	US-10-536-560-186809	Sequence 1

ALIGNMENTS

RESULT 1

US-10-535-164-282627/c

; Sequence 282627, Application US/10535164

; Publication No. US20070134655A1

; GENERAL INFORMATION:

; APPLICANT: BENTWICH, ITZHAK

; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and ther

; FILE REFERENCE: 050992.0200.PCUS13

; CURRENT APPLICATION NUMBER: US/10/535,164

; CURRENT FILING DATE: 2005-05-16

; NUMBER OF SEQ ID NOS: 548156

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 282627

; LENGTH: 32

; TYPE: RNA

; ORGANISM: Human

US-10-535-164-282627

Query Match 8.4%; Score 32; DB 6; Length 32;

Score over Length 100.0%;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 GAGATCTGCTTCAGAGAAATCTTTGGTGT TTT 117

|||||

Db 32 GAGATCTGCTTCAGAGAAATCTTTGGTGT TTT 1

RESULT 2

US-10-536-560-79632/c

; Sequence 79632, Application US/10536560

; Publication No. US20060257851A1

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

; TITLE OF INVENTION: GENES AND USES THEREOF

; FILE REFERENCE: 06087.0300.PCUS13

BLAST Basic Local Alignment Search Tool

Job Title: icl|20482 (379 letters)

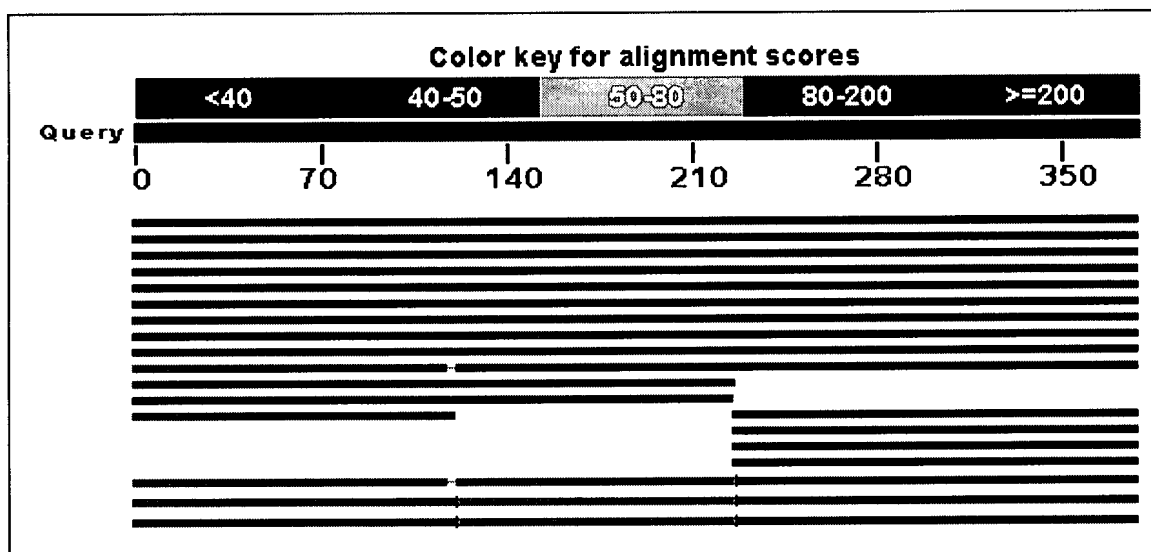
•
•
•

10/7/14, 389

BLASTN 2.2.17 (Aug-26-2007)

RID: M3HBZVH3013 **Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,093,374 sequences; 22,195,605,443 total letters

Query= Length=379

Distribution of 27 Blast Hits on the Query Sequence

Distance tree of results **NEW**

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **R**

Sequences producing significant alignments:

(Click headers to sort columns)

AK292175.1	Homo sapiens cDNA FLJ75783 complete cds, highly similar to Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	701	701	100%	0.0	100%	G
BC146466.1	Synthetic construct Homo sapiens clone IMAGE:100015013, MGC:180176 cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1) mRNA, encodes complete protein	701	701	100%	0.0	100%	G
BC140382.1	Synthetic construct Homo sapiens clone IMAGE:100014401, MGC:173152 cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1) mRNA, encodes complete protein	701	701	100%	0.0	100%	G
AY262056.1	Homo sapiens cytochrome P450 (CYP4Z1) mRNA, complete cds	701	701	100%	0.0	100%	UG
AY358631.1	Homo sapiens clone DNA125150 EPSW3060 (UNQ3060) mRNA, complete cds	701	701	100%	0.0	100%	UG
NM_178134.2	Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	701	701	100%	0.0	100%	UE G
XM_001133951.1	PREDICTED: Homo sapiens cytochrome P450, family 4, subfamily Z, polypeptide 1 (CYP4Z1), mRNA	695	695	100%	0.0	99%	G
AY262057.1	Homo sapiens cytochrome P450 (CYP4Z2P) pseudogene mRNA, complete sequence	645	645	100%	0.0	97%	UG
NR_002788.1	Homo sapiens cytochrome P450 4Z2 pseudogene (CYP4Z2P) on chromosome 1 >dbj AK097373.1 Homo sapiens cDNA FLJ40054 fis, clone TBAES2000315, weakly similar to CYTOCHROME P450 4A1 (EC 1.14.15.3)	645	645	100%	0.0	97%	EG
AY696295.1	Homo sapiens cytochrome P450 (CYP4Z2P) mRNA, complete cds, alternatively spliced	460	646	99%	1e-126	98%	UG
XR_023310.1	PREDICTED: Pan troglodytes similar to cytochrome P450 (LOC456834), mRNA	398	398	59%	1e-107	98%	G
XR_017801.1	PREDICTED: Homo sapiens cytochrome P450 4Z2 pseudogene (CYP4Z2P), misc RNA	374	374	59%	2e-100	96%	G
XM_001175282.1	PREDICTED: Pan troglodytes hypothetical protein LOC750893 (LOC750893), partial mRNA	285	285	40%	9e-74	100%	G
XM_001147911.1	PREDICTED: Pan troglodytes hypothetical protein LOC743794 (LOC743794), partial mRNA	285	285	40%	9e-74	100%	G
AL450996.2	Human DNA sequence from clone RP11-184J23 on chromosome 1 Contains the gene for likely ortholog of rat cytochrome P450 4X1 (CYP4X1), the 5'	285	285	40%	9e-74	100%	

	end of the gene for cytochrome P450 4Z1 (CYP4Z1) and a tubulin alpha pseudogene, complete sequence							
AL731892.6	Human DNA sequence from clone RP11-346M5 on chromosome 1 Contains the 5' end of a cytochrome P450 4Z1 (CYP4Z1) pseudogene, a tubulin alpha pseudogene, the CYP4A11 gene for cytochrome P450 family 4 subfamily A polypeptide 11, complete sequence	285	285	40%	9e-74	100%		
AL356793.19	Human DNA sequence from clone RP4-732G19 on chromosome 1p31.3-32.3 Contains the 3' end of the CYP4B1 gene for cytochrome P450 family 4 subfamily B polypeptide 1 and the 3' end of a cytochrome P450 4Z1 (CYP4Z1) pseudogene, complete sequence	285	651	99%	9e-74	100%		
AL135960.1	Human DNA sequence from clone RP1-18D14 on chromosome 1 Contains the 3' end of the gene for cytochrome P450 4Z1 (CYP4Z1), the gene for a novel protein similar to cytochrome P450 family 4 subfamily A polypeptide 11 (CYP4A11) (LOC284541), a NADH dehydrogenase 1 mitochondrial pseudogene, three novel genes, the gene for membrane-associated protein 17 (MAP17), the TAL1 gene for T-cell acute lymphocytic leukemia 1, the 3' end of the SIL gene for TAL1 (SCL) interrupting locus and a CpG island, complete sequence	285	706	100%	9e-74	100%	E	
AJ131016.1	Homo sapiens SCL gene locus	285	706	100%	9e-74	100%	E	
AC203188.3	Rhesus Macaque BAC CH250-61I12 () complete sequence	202	202	31%	9e-49	96%		